

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/574,129
Source: IFWP
Date Processed by STIC: 4-13-06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/13/2006

PATENT APPLICATION: US/10/574,129

TIME: 10:02:54

Input Set : F:\180-179 PCT.ST25.txt

Output Set: N:\CRF4\04132006\J574129.raw

3 <110> APPLICANT: Li, Chuan-Yuan
 4 Zhang, Xiuwu
 5 Dewhirst, Mark W
 7 <120> TITLE OF INVENTION: A NOVEL siRNA-BASED APPROACH TO TARGET THE HIF-ALPHA FACTOR
 FOR
 8 GENE THERAPY
 10 <130> FILE REFERENCE: 180-179 PCT
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/574,129
 C--> 12 <141> CURRENT FILING DATE: 2006-03-31
 12 <150> PRIOR APPLICATION NUMBER: US 60/508,145
 13 <151> PRIOR FILING DATE: 2003-10-02
 15 <160> NUMBER OF SEQ ID NOS: 12
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 3958
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (285)..(2765)
 29 <400> SEQUENCE: 1
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 34 ttgccgcccg cttctctcta gtctcacgag gggtttcccg cctcgacccc ccacctctgg 180
 36 acttgccctt cttctctctt tccgcgtgtg gagggagcca gcgcttaggc cggagcgcgc 240
 38 ctggggggccg cccgccgtga agacatcgcg gggaccgatt cacc atg gag ggc gcc 296
 39 Met Glu Gly Ala
 40 1
 42 ggc ggc gcg aac gac aag aaa aag ata agt tct gaa cgt cga aaa gaa 344
 43 Gly Gly Ala Asn Asp Lys Lys Lys Ile Ser Ser Glu Arg Arg Lys Glu
 44 5 10 15 20
 46 aag tct cga gat gca gcc aga tct cgg cga agt aaa gaa tct gaa gtt 392
 47 Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys Glu Ser Glu Val
 48 25 30 35
 50 ttt tat gag ctt gct cat cag ttg cca ctt cca cat aat gtg agt tcg 440
 51 Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His Asn Val Ser Ser
 52 40 45 50
 54 cat ctt gat aag gcc tct gtg atg agg ctt acc atc agc tat ttg cgt 488
 55 His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile Ser Tyr Leu Arg
 56 55 60 65
 58 gtg agg aaa ctt ctg gat gct ggt gat ttg gat att gaa gat gac atg 536
 59 Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile Glu Asp Asp Met
 60 70 75 80
 62 aaa gca cag atg aat tgc ttt tat ttg aaa gcc ttg gat ggt ttt gtt 584

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| 63 | Lys | Ala | Gln | Met | Asn | Cys | Phe | Tyr | Leu | Lys | Ala | Leu | Asp | Gly | Phe | Val | |
| 64 | 85 | | | | 90 | | | | | 95 | | | | | | 100 | |
| 66 | atg | gtt | ctc | aca | gat | gat | ggt | gac | atg | att | tac | att | tct | gat | aat | gtg | 632 |
| 67 | Met | Val | Leu | Thr | Asp | Asp | Gly | Asp | Met | Ile | Tyr | Ile | Ser | Asp | Asn | Val | |
| 68 | | | | | 105 | | | | | 110 | | | | | 115 | | |
| 70 | aac | aaa | tac | atg | gga | tta | act | cag | ttt | gaa | cta | act | gga | cac | agt | gtg | 680 |
| 71 | Asn | Lys | Tyr | Met | Gly | Leu | Thr | Gln | Phe | Glu | Leu | Thr | Gly | His | Ser | Val | |
| 72 | | | | 120 | | | | | 125 | | | | | 130 | | | |
| 74 | ttt | gat | ttt | act | cat | cca | tgt | gac | cat | gag | gaa | atg | aga | gaa | atg | ctt | 728 |
| 75 | Phe | Asp | Phe | Thr | His | Pro | Cys | Asp | His | Glu | Glu | Met | Arg | Glu | Met | Leu | |
| 76 | | | 135 | | | | | 140 | | | | | 145 | | | | |
| 78 | aca | cac | aga | aat | ggc | ctt | gtg | aaa | aag | ggt | aaa | gaa | caa | aac | aca | cag | 776 |
| 79 | Thr | His | Arg | Asn | Gly | Leu | Val | Lys | Lys | Gly | Lys | Glu | Gln | Asn | Thr | Gln | |
| 80 | | 150 | | | | | 155 | | | | | 160 | | | | | |
| 82 | cga | agc | ttt | ttt | ctc | aga | atg | aag | tgt | acc | cta | act | agc | cga | gga | aga | 824 |
| 83 | Arg | Ser | Phe | Phe | Leu | Arg | Met | Lys | Cys | Thr | Leu | Thr | Ser | Arg | Gly | Arg | |
| 84 | 165 | | | | | 170 | | | | 175 | | | | | 180 | | |
| 86 | act | atg | aac | ata | aag | tct | gca | aca | tgg | aag | gta | ttg | cac | tgc | aca | ggc | 872 |
| 87 | Thr | Met | Asn | Ile | Lys | Ser | Ala | Thr | Trp | Lys | Val | Leu | His | Cys | Thr | Gly | |
| 88 | | | | 185 | | | | | | 190 | | | | | 195 | | |
| 90 | cac | att | cac | gta | tat | gat | acc | aac | agt | aac | caa | cct | cag | tgt | ggg | tat | 920 |
| 91 | His | Ile | His | Val | Tyr | Asp | Thr | Asn | Ser | Asn | Gln | Pro | Gln | Cys | Gly | Tyr | |
| 92 | | | | 200 | | | | | 205 | | | | | 210 | | | |
| 94 | aag | aaa | cca | cct | atg | acc | tgc | ttg | gtg | ctg | att | tgt | gaa | ccc | att | cct | 968 |
| 95 | Lys | Lys | Pro | Pro | Met | Thr | Cys | Leu | Val | Leu | Ile | Cys | Glu | Pro | Ile | Pro | |
| 96 | | | 215 | | | | 220 | | | | | 225 | | | | | |
| 98 | cac | cca | tca | aat | att | gaa | att | cct | tta | gat | agc | aag | act | ttc | ctc | agt | 1016 |
| 99 | His | Pro | Ser | Asn | Ile | Glu | Ile | Pro | Leu | Asp | Ser | Lys | Thr | Phe | Leu | Ser | |
| 100 | | 230 | | | | | 235 | | | | | 240 | | | | | |
| 102 | cga | cac | agc | ctg | gat | atg | aaa | ttt | tct | tat | tgt | gat | gaa | aga | att | acc | 1064 |
| 103 | Arg | His | Ser | Leu | Asp | Met | Lys | Phe | Ser | Tyr | Cys | Asp | Glu | Arg | Ile | Thr | |
| 104 | 245 | | | | | 250 | | | | | 255 | | | | 260 | | |
| 106 | gaa | ttg | atg | gga | tat | gag | cca | gaa | gaa | ctt | tta | ggc | cgc | tca | att | tat | 1112 |
| 107 | Glu | Leu | Met | Gly | Tyr | Glu | Pro | Glu | Glu | Leu | Leu | Gly | Arg | Ser | Ile | Tyr | |
| 108 | | | | 265 | | | | | 270 | | | | | 275 | | | |
| 110 | gaa | tat | tat | cat | gct | ttg | gac | tct | gat | cat | ctg | acc | aaa | act | cat | cat | 1160 |
| 111 | Glu | Tyr | Tyr | His | Ala | Leu | Asp | Ser | Asp | His | Leu | Thr | Lys | Thr | His | His | |
| 112 | | | | 280 | | | | | 285 | | | | | 290 | | | |
| 114 | gat | atg | ttt | act | aaa | gga | caa | gtc | acc | aca | gga | cag | tac | agg | atg | ctt | 1208 |
| 115 | Asp | Met | Phe | Thr | Lys | Gly | Gln | Val | Thr | Thr | Gly | Gln | Tyr | Arg | Met | Leu | |
| 116 | | | 295 | | | | 300 | | | | | 305 | | | | | |
| 118 | gcc | aaa | aga | ggg | gga | tat | gtc | tgg | gtt | gaa | act | caa | gca | act | gtc | ata | 1256 |
| 119 | Ala | Lys | Arg | Gly | Gly | Tyr | Val | Trp | Val | Glu | Thr | Gln | Ala | Thr | Val | Ile | |
| 120 | | 310 | | | | | 315 | | | | | 320 | | | | | |
| 122 | tat | aac | acc | aag | aat | tct | caa | cca | cag | tgc | att | gta | tgt | gtg | aat | tac | 1304 |
| 123 | Tyr | Asn | Thr | Lys | Asn | Ser | Gln | Pro | Gln | Cys | Ile | Val | Cys | Val | Asn | Tyr | |
| 124 | 325 | | | | | 330 | | | | 335 | | | | | 340 | | |
| 126 | gtt | gtg | agt | ggg | att | att | cag | cac | gac | ttg | att | ttc | tcc | ctt | caa | caa | 1352 |
| 127 | Val | Val | Ser | Gly | Ile | Ile | Gln | His | Asp | Leu | Ile | Phe | Ser | Leu | Gln | Gln | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 128 | | | | 345 | | | | 350 | | | | 355 | | | | |
| 130 | aca | gaa | tgt | gtc | ctt | aaa | ccg | ggt | gaa | tct | tca | gat | atg | aaa | atg | act |
| 131 | Thr | Glu | Cys | Val | Leu | Lys | Pro | Val | Glu | Ser | Ser | Asp | Met | Lys | Met | Thr |
| 132 | | | | 360 | | | | 365 | | | | 370 | | | | |
| 134 | cag | cta | ttc | acc | aaa | ggt | gaa | tca | gaa | gat | aca | agt | agc | ctc | ttt | gac |
| 135 | Gln | Leu | Phe | Thr | Lys | Val | Glu | Ser | Glu | Asp | Thr | Ser | Ser | Leu | Phe | Asp |
| 136 | | | 375 | | | | 380 | | | | 385 | | | | | |
| 138 | aaa | ctt | aag | aag | gaa | cct | gat | gct | tta | act | ttg | ctg | gcc | cca | gcc | gct |
| 139 | Lys | Leu | Lys | Lys | Glu | Pro | Asp | Ala | Leu | Thr | Leu | Leu | Ala | Pro | Ala | Ala |
| 140 | | 390 | | | | | 395 | | | | 400 | | | | | |
| 142 | gga | gac | aca | atc | ata | tct | tta | gat | ttt | ggc | agc | aac | gac | aca | gaa | act |
| 143 | Gly | Asp | Thr | Ile | Ile | Ser | Leu | Asp | Phe | Gly | Ser | Asn | Asp | Thr | Glu | Thr |
| 144 | 405 | | | | 410 | | | | 415 | | | | 420 | | | |
| 146 | gat | gac | cag | caa | ctt | gag | gaa | gta | cca | tta | tat | aat | gat | gta | atg | ctc |
| 147 | Asp | Asp | Gln | Gln | Leu | Glu | Glu | Val | Pro | Leu | Tyr | Asn | Asp | Val | Met | Leu |
| 148 | | | | 425 | | | | 430 | | | | 435 | | | | |
| 150 | ccc | tca | ccc | aac | gaa | aaa | tta | cag | aat | ata | aat | ttg | gca | atg | tct | cca |
| 151 | Pro | Ser | Pro | Asn | Glu | Lys | Leu | Gln | Asn | Ile | Asn | Leu | Ala | Met | Ser | Pro |
| 152 | | | 440 | | | | | 445 | | | | 450 | | | | |
| 154 | tta | ccc | acc | gct | gaa | acg | cca | aag | cca | ctt | cga | agt | agt | gct | gac | cct |
| 155 | Leu | Pro | Thr | Ala | Glu | Thr | Pro | Lys | Pro | Leu | Arg | Ser | Ser | Ala | Asp | Pro |
| 156 | | | 455 | | | | 460 | | | | 465 | | | | | |
| 158 | gca | ctc | aat | caa | gaa | ggt | gca | tta | aaa | tta | gaa | cca | aat | cca | gag | tca |
| 159 | Ala | Leu | Asn | Gln | Glu | Val | Ala | Leu | Lys | Leu | Glu | Pro | Asn | Pro | Glu | Ser |
| 160 | | 470 | | | | 475 | | | 480 | | | | | | | |
| 162 | ctg | gaa | ctt | tct | ttt | acc | atg | ccc | cag | att | cag | gat | cag | aca | cct | agt |
| 163 | Leu | Glu | Leu | Ser | Phe | Thr | Met | Pro | Gln | Ile | Gln | Asp | Gln | Thr | Pro | Ser |
| 164 | 485 | | | | 490 | | | | 495 | | | | 500 | | | |
| 166 | cct | tcc | gat | gga | agc | act | aga | caa | agt | tca | cct | gag | cct | aat | agt | ccc |
| 167 | Pro | Ser | Asp | Gly | Ser | Thr | Arg | Gln | Ser | Ser | Pro | Glu | Pro | Asn | Ser | Pro |
| 168 | | | | 505 | | | | 510 | | | | 515 | | | | |
| 170 | agt | gaa | tat | tgt | ttt | tat | gtg | gat | agt | gat | atg | gtc | aat | gaa | ttc | aag |
| 171 | Ser | Glu | Tyr | Cys | Phe | Tyr | Val | Asp | Ser | Asp | Met | Val | Asn | Glu | Phe | Lys |
| 172 | | | 520 | | | | | 525 | | | | 530 | | | | |
| 174 | ttg | gaa | ttg | gta | gaa | aaa | ctt | ttt | gct | gaa | gac | aca | gaa | gca | aag | aac |
| 175 | Leu | Glu | Leu | Val | Glu | Lys | Leu | Phe | Ala | Glu | Asp | Thr | Glu | Ala | Lys | Asn |
| 176 | | | 535 | | | | | 540 | | | | 545 | | | | |
| 178 | cca | ttt | tct | act | cag | gac | aca | gat | tta | gac | ttg | gag | atg | tta | gct | ccc |
| 179 | Pro | Phe | Ser | Thr | Gln | Asp | Thr | Asp | Leu | Asp | Leu | Glu | Met | Leu | Ala | Pro |
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| 182 | tat | atc | cca | atg | gat | gat | gac | ttc | cag | tta | cgt | tcc | ttc | gat | cag | ttg |
| 183 | Tyr | Ile | Pro | Met | Asp | Asp | Asp | Phe | Gln | Leu | Arg | Ser | Phe | Asp | Gln | Leu |
| 184 | 565 | | | | 570 | | | | 575 | | | | 580 | | | |
| 186 | tca | cca | tta | gaa | agc | agt | tcc | gca | agc | cct | gaa | agc | gca | agt | cct | caa |
| 187 | Ser | Pro | Leu | Glu | Ser | Ser | Ser | Ala | Ser | Pro | Glu | Ser | Ala | Ser | Pro | Gln |
| 188 | | | | 585 | | | | 590 | | | | 595 | | | | |
| 190 | agc | aca | ggt | aca | gta | ttc | cag | cag | act | caa | ata | caa | gaa | cct | act | gct |
| 191 | Ser | Thr | Val | Thr | Val | Phe | Gln | Gln | Thr | Gln | Ile | Gln | Glu | Pro | Thr | Ala |
| 192 | | | | 600 | | | | 605 | | | | 610 | | | | |

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196      615      620      625
198 aaa gac cgt atg gaa gac att aaa ata ttg att gca tct cca tct cct      2216
199 Lys Asp Arg Met Glu Asp Ile Lys Ile Leu Ile Ala Ser Pro Ser Pro
200      630      635      640
202 acc cac ata cat aaa gaa act act agt gcc aca tca tca cca tat aga      2264
203 Thr His Ile His Lys Glu Thr Thr Ser Ala Thr Ser Ser Pro Tyr Arg
204 645      650      655      660
206 gat act caa agt cgg aca gcc tca cca aac aga gca gga aaa gga gtc      2312
207 Asp Thr Gln Ser Arg Thr Ala Ser Pro Asn Arg Ala Gly Lys Gly Val
208      665      670      675
210 ata gaa cag aca gaa aaa tct cat cca aga agc cct aac gtg tta tct      2360
211 Ile Glu Gln Thr Glu Lys Ser His Pro Arg Ser Pro Asn Val Leu Ser
212      680      685      690
214 gtc gct ttg agt caa aga act aca gtt cct gag gaa gaa cta aat cca      2408
215 Val Ala Leu Ser Gln Arg Thr Thr Val Pro Glu Glu Glu Leu Asn Pro
216      695      700      705
218 aag ata cta gct ttg cag aat gct cag aga aag cga aaa atg gaa cat      2456
219 Lys Ile Leu Ala Leu Gln Asn Ala Gln Arg Lys Arg Lys Met Glu His
220      710      715      720
222 gat ggt tca ctt ttt caa gca gta gga att gga aca tta tta cag cag      2504
223 Asp Gly Ser Leu Phe Gln Ala Val Gly Ile Gly Thr Leu Leu Gln Gln
224 725      730      735      740
226 cca gac gat cat gca gct act aca tca ctt tct tgg aaa cgt gta aaa      2552
227 Pro Asp Asp His Ala Ala Thr Thr Ser Leu Ser Trp Lys Arg Val Lys
228      745      750      755
230 gga tgc aaa tct agt gaa cag aat gga atg gag caa aag aca att att      2600
231 Gly Cys Lys Ser Ser Glu Gln Asn Gly Met Glu Gln Lys Thr Ile Ile
232      760      765      770
234 tta ata ccc tct gat tta gca tgt aga ctg ctg ggg caa tca atg gat      2648
235 Leu Ile Pro Ser Asp Leu Ala Cys Arg Leu Leu Gly Gln Ser Met Asp
236      775      780      785
238 gaa agt gga tta cca cag ctg acc agt tat gat tgt gaa gtt aat gct      2696
239 Glu Ser Gly Leu Pro Gln Leu Thr Ser Tyr Asp Cys Glu Val Asn Ala
240      790      795      800
242 cct ata caa ggc agc aga aac cta ctg cag ggt gaa gaa tta ctc aga      2744
243 Pro Ile Gln Gly Ser Arg Asn Leu Leu Gln Gly Glu Glu Leu Leu Arg
244 805      810      815      820
246 gct ttg gat caa gtt aac tga gctttttctt aatttcattc ctttttttgg      2795
247 Ala Leu Asp Gln Val Asn
248      825
250 aactggtgg ctactacct aaagcagtct atttatattt tctacatcta attttagaag      2855
252 cctggctaca atactgcaca aacttggtta gttcaatttt tgatcccctt tctacttaat      2915
254 ttacattaat gctctttttt agtatgttct ttaatgctgg atcacagaca gctcattttc      2975
256 tcagtttttt ggtatttaaa ccattgcatt gcagtagcat catttttaaaa aatgcacctt      3035
258 tttattttatt tatttttggc tagggagttt atcccttttt cgaattattt ttaagaagat      3095
260 gccaatataa tttttgtaag aaggcagtaa cttttcatca tgatcatagg cagttgaaaa      3155
262 attttttacac cttttttttc acattttaca taaataataa tgctttgcca gcagtagctg      3215

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268 acctggaaca tgacattggt aatcatataa taatgattct taaatgctgt atggtttatt 3395
270 atttaaattgg gtaaagccat ttacataata tagaaagata tgcataatc tagaaggatc 3455
272 gtggcattta ttgggataaa attctcaatt cagagaaatc atctgatgtt tctatagtca 3515
274 ctttgccagc tcaaaagaaa acaataccct atgtagtgtt ggaagtttat gctaattattg 3575
276 tgtaactgat attaaaccta aatgttctgc ctaccctgtt ggtataaaga tattttgagc 3635
278 agactgtaaa caagaaaaaa aaaatcatgc attcttagca aaattgccta gtatgttaat 3695
280 ttgctcaaaa tacaatgttt gattttatgc actttgtcgc tattaacatc ctttttttca 3755
282 tgtagatttc aataattgag taattttaga agcattatct taggaatata tagttgtcac 3815
284 agtaaataatc ttgttttttc tatgtacatt gtacaaatct ttcattcctt ttgctctttg 3875
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288 caggaaaaaa aaaaaaaaaa aaa 3958
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293 <212> TYPE: PRT
294 <213> ORGANISM: Homo sapiens
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302 Arg Arg Lys Glu Lys Ser Arg Asp Ala Arg Ser Arg Arg Ser Lys
303 20 25 30
306 Glu Ser Glu Val Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His
307 35 40 45
310 Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile
311 50 55 60
314 Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile
315 65 70 75 80
318 Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu
319 85 90 95
322 Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile
323 100 105 110
326 Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr
327 115 120 125
330 Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met
331 130 135 140
334 Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu
335 145 150 155 160
338 Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr
339 165 170 175
342 Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu
343 180 185 190
346 His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro
347 195 200 205
350 Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys
351 210 215 220
354 Glu Pro Ile Pro His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys
355 225 230 235 240
358 Thr Phe Leu Ser Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 20,21,22,23,24,25,26,27,28,48,49,50,51,52,53,54,55

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,8

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0